

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	3361.5	74.9	841	2	US-09-897-427A-2		Sequence 2, Appli
2	1456.5	32.5	839	2	US-09-897-427A-4		Sequence 4, Appli
3	1428	31.8	843	2	US-09-361-631-1		Sequence 1, Appli
4	1425	31.8	843	2	US-09-361-631-2		Sequence 2, Appli
5	1208.5	26.9	852	2	US-09-897-427A-6		Sequence 6, Appli
6	1163.5	25.9	1059	2	US-09-134-513-2		Sequence 2, Appli
7	1157	25.8	669	2	US-09-361-631-7		Sequence 7, Appli
8	1146	25.6	1078	1	US-08-485-588-7		Sequence 7, Appli
9	1146	25.6	1078	1	US-08-484-565-7		Sequence 7, Appli
10	1146	25.6	1078	1	US-08-480-751-7		Sequence 7, Appli
11	1146	25.6	1078	1	US-08-943-986-7		Sequence 7, Appli
12	1146	25.6	1078	2	US-08-353-784-7		Sequence 7, Appli
13	1146	25.6	1078	2	US-08-484-719B-7		Sequence 7, Appli
14	1146	25.6	1078	2	US-08-484-153-7		Sequence 7, Appli
15	1144.5	25.5	1085	1	US-08-485-588-5		Sequence 5, Appli
16	1144.5	25.5	1085	1	US-08-484-565-5		Sequence 5, Appli
17	1144.5	25.5	1085	1	US-08-480-751-5		Sequence 5, Appli
18	1144.5	25.5	1085	1	US-08-943-986-5		Sequence 5, Appli
19	1144.5	25.5	1085	2	US-08-353-784-5		Sequence 5, Appli
20	1144.5	25.5	1085	2	US-08-484-719B-5		Sequence 5, Appli
21	1144.5	25.5	1085	2	US-08-484-153-5		Sequence 5, Appli
22	1134	25.3	1088	1	US-08-485-588-6		Sequence 6, Appli
23	1134	25.3	1088	1	US-08-484-565-6		Sequence 6, Appli
24	1134	25.3	1088	1	US-08-480-751-6		Sequence 6, Appli
25	1134	25.3	1088	1	US-08-943-986-6		Sequence 6, Appli
26	1134	25.3	1088	2	US-08-353-784-6		Sequence 6, Appli
27	1134	25.3	1088	2	US-08-484-719B-6		Sequence 6, Appli

GenCore version 5.1.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: May 4, 2006, 14:52:34 ; Search time 100.773 Seconds
(without alignments)
3482.855 Million cell updates/sec
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Perfect score: 4485
Sequence: 1 MLFWAAHLLLSLQVYCWAF.....NNTFHQASIQDYTRRCGTT 840
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1867569 seqs, 417829326 residues
Total number of hits satisfying chosen parameters: 1867569
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
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3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pcp:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pcp:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pcp:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4485	100.0	840	3	US-09-361-652-1 Sequence 1, Appli
2	4485	100.0	840	3	US-09-361-652-1 Sequence 1, Appli
3	4485	100.0	840	4	US-10-246-785-3 Sequence 3, Appli
4	4485	100.0	840	4	US-10-190-417-1 Sequence 1, Appli
5	4485	100.0	840	4	US-10-159-339-12 Sequence 12, Appli
6	4485	100.0	840	4	US-10-179-373-16 Sequence 16, Appli
7	4485	100.0	840	4	US-10-436-715-39 Sequence 39, Appli
8	4485	100.0	840	4	US-10-436-715-69 Sequence 69, Appli
9	4485	100.0	840	4	US-10-725-103-16 Sequence 16, Appli
10	4485	100.0	840	4	US-10-725-489-16 Sequence 16, Appli
11	4485	100.0	840	4	US-10-725-080A-16 Sequence 16, Appli
12	4485	100.0	840	4	US-10-725-472A-16 Sequence 16, Appli
13	4485	100.0	840	5	US-10-725-418-16 Sequence 16, Appli
14	4485	100.0	840	5	US-10-679-102-1 Sequence 1, Appli
15	4123	91.9	842	4	US-10-436-715-35 Sequence 35, Appli
16	4123	91.9	842	4	US-10-436-715-67 Sequence 67, Appli
17	4100	91.4	842	3	US-09-361-652-2 Sequence 2, Appli
18	4100	91.4	842	3	US-09-361-652-2 Sequence 2, Appli
19	4100	91.4	842	4	US-10-246-785-2 Sequence 2, Appli
20	4100	91.4	842	4	US-10-190-417-2 Sequence 2, Appli
21	4100	91.4	842	5	US-10-679-102-2 Sequence 2, Appli
22	4078	90.9	842	4	US-10-436-715-68 Sequence 68, Appli
23	4026.5	89.8	1138	4	US-10-261-482-4 Sequence 4, Appli
24	3364	75.0	840	4	US-10-190-417-3 Sequence 3, Appli
25	3364	75.0	840	5	US-10-679-102-3 Sequence 3, Appli
26	3362.5	75.0	841	4	US-10-188-186-2 Sequence 2, Appli
27	3361.5	74.9	841	3	US-09-819-946-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-361-652-1
; Sequence 1, Application US/09361652
; Publication No. US2003036630A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Lindemeier, Juergen
; APPLICANT: Ryba, Nick
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor
; TITLE OF INVENTION: Involved in Sensory Transduction
; FILE REFERENCE: 023078-088610US
; CURRENT APPLICATION NUMBER: US/09/361,652
; CURRENT FILING DATE: 1999-07-27
; EARLIER APPLICATION NUMBER: US 60/094,465
; EARLIER FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 840
; TYPE: PRT
; ORGANISM: Rattus sp.
; FEATURE:
; OTHER INFORMATION: rat G-protein coupled receptor B3 (GPCR-B3)
US-09-361-652-1
Query Match 100.0%; Score 4485; DB 3; Length 840;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 840; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MLFWAAHLLLSLQVYCWAFSCORTSSPGFSLPGDPLAGLPSLHGDCQLQVRRPLVTS 60
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Db 61 CDRPDSFNGHGHLFOAMFTVEEINNSALLPNITLGYELDYVCSESANVYATLRVAL 120
QY 121 QGPRHTEIOKDLRNHSSKVVAFIGPDNTDHAVTAAALGPFLMPLVSYEASSVVLVSAKRK 180
Db 121 QGPRHTEIOKDLRNHSSKVVAFIGPDNTDHAVTAAALGPFLMPLVSYEASSVVLVSAKRK 180
QY 181 FPSFLRTVPSDRHQVVMVQLQSGFQVWISLIGSYGDIQQLGVQALAEELAVPRGICVAF 240
Db 181 FPSFLRTVPSDRHQVVMVQLQSGFQVWISLIGSYGDIQQLGVQALAEELAVPRGICVAF 240
QY 241 KDIIVPSARVGDPRMSMQHQAQRTVVVVSNEHLARVFRSVVLANTLCTGVVWASE 300
Db 241 KDIIVPSARVGDPRMSMQHQAQRTVVVVSNEHLARVFRSVVLANTLCTGVVWASE 300

Dd	241	KDIPFSARVGDPRMQSMQHQAARTT	300
Qy	301	DWAISTYTSVTGIGIGITVGVAVQORQVPG	360
Dd	301	DWAISTYTSVTGIGIGITVGVAVQORQVPG	360
Qy	361	OLCRECHTFTTRNMPITLGAFAFSAARVVEA	420
Dd	361	OLCRECHTFTTRNMPITLGAFAFSAARVVEA	420
Qy	421	LOQIYKVNFLHENTVAFDDNGDITLGYDII	480
Dd	421	LOQIYKVNFLHENTVAFDDNGDITLGYDII	480
Qy	481	KIOWHGKNNQVPSVCTTDLGAGHRVVGSHH	540
Dd	481	KIOWHGKNNQVPSVCTTDLGAGHRVVGSHH	540
Qy	541	EWAPKESSTCPRVTEFLAWHEPISLVLIANT	600
Dd	541	EWAPKESSTCPRVTEFLAWHEPISLVLIANT	600
Qy	601	GRCLFMLGSLVAGSCSFYFSGEPTVPACLRQ	660
Dd	601	GRCLFMLGSLVAGSCSFYFSGEPTVPACLRQ	660
Qy	661	FSTKVTFTYRTWAQNHGAGLFVIVSSTVHL	720
Dd	661	FSTKVTFTYRTWAQNHGAGLFVIVSSTVHL	720
Qy	721	EYNSVGFLLAFTNILLSTFVCSYLGKELPEN	780
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US-09-927-315-1			
; Sequence 1, Application US/09927315			
; Publication No. US20030040045A1			
; GENERAL INFORMATION:			
; APPLICANT: Zuker, Charles S.			
; APPLICANT: Ryba, Nicholas J.P.			
; APPLICANT: Nelson, Greg			
; APPLICANT: Hoon, Mark A.			
; APPLICANT: Chandrasekhar, Jayaram			
; APPLICANT: Zhang, Yifeng			
; APPLICANT: The Regents of the University of California			
; APPLICANT: The Government of the United States of America			
; APPLICANT: as represented by the Secretary of the			
; APPLICANT: Department of Health and Human Services			
; TITLE OF INVENTION: Mammalian Sweet Taste Receptors			
; FILE REFERENCE: 02307E-120110US			
; CURRENT APPLICATION NUMBER: US/09/927,315			
; PRIOR FILING DATE: 2001-08-10			
; PRIOR APPLICATION NUMBER: US 60/302,898			
; NUMBER OF SEQ ID NOS: 25			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 1			
; LENGTH: 840			
; TYPE: PRT			
; ORGANISM: Rattus sp.			
; FEATURE:			
; OTHER INFORMATION: rat T1r1 sweet taste receptor			
US-09-927-315-1			
Query Match 100.0%; Score 4485; DB 3; Length 840;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 840; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			

GenCore version 5.1.7
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(without alignments)
2421.578 Million cell updates/sec

Title: US-09-361-652-1
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Sequence: 1 MLFWAHLHLLSLQVYCWAF.....NNTFHQASIQDYTRCGTT 840

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 6: /SIDSS/ptodata/2/pubpaa/US09_NEW_PUB.pep1.*
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- 12: /SIDSS/ptodata/2/pubpaa/US16_NEW_PUB.pep1.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4485	100.0	840	9	US-10-645-441-1
2	4485	100.0	840	9	US-10-725-475-16
3	4100	91.4	842	9	US-10-645-441-2
4	3361.5	74.9	841	11	US-10-725-475-5
5	3361.5	74.9	841	11	US-11-050-804-2
6	3154.5	70.3	777	9	US-10-645-441-3
7	1456.5	32.5	839	9	US-10-725-475-6
8	1456.5	32.5	839	11	US-11-050-804-4
9	1454	32.4	838	9	US-10-645-441-9
10	1428	31.8	843	9	US-10-645-441-7
11	1428	31.8	843	9	US-10-725-475-17
12	1425	31.8	843	9	US-10-645-441-8
13	1211.5	27.0	852	9	US-10-725-475-7
14	1208.5	26.9	852	9	US-10-645-441-15
15	1208.5	26.9	852	11	US-11-050-804-6
16	1197	26.7	858	9	US-10-645-441-25
17	1197	26.7	858	9	US-10-725-475-4
18	1189.5	26.5	858	9	US-10-645-441-18
19	1185.5	26.4	858	9	US-10-645-441-23
20	1180.5	26.3	858	9	US-10-645-441-20
21	1138	25.4	867	9	US-10-725-475-19

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Sequence 6, Appli
Sequence 2, Appli
Sequence 15, Appli
Sequence 18, Appli
Sequence 17, Appli
Sequence 53, Appli
Sequence 54, Appli
Sequence 41, Appli
Sequence 52, Appli
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Sequence 8, Appli
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Sequence 20, Appli
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Sequence 40, Appli
Sequence 2, Appli

22 1079 24.1 928 9 US-10-841-129-4
23 1061 23.7 928 9 US-10-841-129-6
24 1023 22.8 926 9 US-10-841-129-2
25 731 16.3 1199 9 US-10-922-166-15
26 728 16.2 845 9 US-10-725-475-18
27 719 16.0 879 9 US-10-877-346-17
28 714 15.9 879 9 US-10-877-346-53
29 713 15.9 879 9 US-10-877-346-54
30 712.5 15.9 865 11 US-11-094-519A-41
31 710.5 15.8 879 9 US-10-877-346-52
32 476.5 10.6 242 9 US-10-725-475-13
33 447.5 10.0 497 9 US-10-918-857-8
34 447.5 10.0 576 9 US-10-922-166-2
35 447.5 10.0 790 9 US-10-918-857-6
36 447.5 10.0 790 9 US-10-922-166-20
37 388 8.7 425 9 US-10-918-857-4
38 388 8.7 718 9 US-10-918-857-2
39 381.5 8.5 256 9 US-10-877-346-85
40 375 8.4 236 9 US-10-725-475-15
41 326.5 7.3 165 9 US-10-725-475-14
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43 284 6.3 402 9 US-10-877-346-84
44 177.5 4.0 844 11 US-11-127-877-40
45 165.5 3.7 885 9 US-10-912-971-2

ALIGNMENTS

RESULT 1

US-10-645-441-1

; Sequence 1, Application US/10645441
; Publication No. US20050260599A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Ryba, Nicholas J.P.
; APPLICANT: Nelson, Greg
; APPLICANT: Hoon, Mark A.
; APPLICANT: Chandrasekar, Jayaram
; APPLICANT: Zhang, Yifeng
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Mammalian Sweet Taste Receptors
; FILE REFERENCE: 02307E-120110US
; CURRENT APPLICATION NUMBER: US/10/645,441
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: US/09/927,315
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/302,898
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 840
; TYPE: PRT
; ORGANISM: Rattus sp.
; FEATURE:
; OTHER INFORMATION: rat Tir1 sweet taste receptor
US-10-645-441-1

Query Match 100.0%; Score 4485; DB 9; Length 840;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 840; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MLFWAHLHLLSLQVYCWAFSCORTSSPGFSLPGDFLLAGLSLHDCDCLQVHRPLVTS 60
Qy 61 CDRPDSFNGHYHLFOAMRTVEEINNSSALLPNITLGYELDYVCSANVYATLRVLL 120
Db 61 CDRPDSFNGHYHLFOAMRTVEEINNSSALLPNITLGYELDYVCSANVYATLRVLL 120

QY 121 QGPRHIEIQKDLRNHSSKVAFIPGPDNDTHAVTTAALGPFLLMPLVSVYEAASSVLSAKRK 180
DB 121 QGPRHIEIQKDLRNHSSKVAFIPGPDNDTHAVTTAALGPFLLMPLVSVYEAASSVLSAKRK 180
QY 181 PFSFLRTVPSDRHQVEVMVQLQSGFWWISLIGSYGDIYGVQALBELAVPRGICVAF 240
DB 181 PFSFLRTVPSDRHQVEVMVQLQSGFWWISLIGSYGDIYGVQALBELAVPRGICVAF 240
QY 241 KDIVPFSARVGDPRMQSMQHLAQARTTVVVVFSNRHLARVFRSVVLANTLTKGVWASE 300
DB 241 KDIVPFSARVGDPRMQSMQHLAQARTTVVVVFSNRHLARVFRSVVLANTLTKGVWASE 300
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DB 301 DWAISTYITSVTGIQIGITVLGVAVQOQVPGKKEFEESYVRAVTAAPSACPEGSWCSTN 360
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DB 361 QLCRECHTFTTRNMPTLGAFAFSAAYRVYEAHVAVAGHLQLLGCTSEICSRGPVYPWOL 420
QY 421 LQOIYKVNFLHENTVAFDDNGDTLGYDDI IAWDNMGPEWTTEIIGSASLSPVHLDINKT 480
DB 421 LQOIYKVNFLHENTVAFDDNGDTLGYDDI IAWDNMGPEWTTEIIGSASLSPVHLDINKT 480
QY 481 KIOWHGKNNQVPSVCTTDCLAGHRVWVSHHCCFECVPCBAGTFLNMSLHIQPCGCT 540
DB 481 KIOWHGKNNQVPSVCTTDCLAGHRVWVSHHCCFECVPCBAGTFLNMSLHIQPCGCT 540
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DB 721 EYNSVGFLLAFTHNILLSTSTFVCSYLKGLPENYNEAKCVTFSLNLFVSWIAPFTMAS 780
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DB 781 IYQGSYLPVAVNLAGITLISGGFSGYFLPKCVYILCRPELNTEHPQASIQDYTRCGTT 840

RESULT 2

US-10-725-475-16
; Sequence 16, Application US/10725475
; Publication No. US20060014208A1
; GENERAL INFORMATION:
; APPLICANT: ZOLLER, MARK
; APPLICANT: LI, XIAODONG
; APPLICANT: STASZEWSKI, LENA
; APPLICANT: O'CONNELL, SHAWN
; APPLICANT: ZOZULYA, SERGEY
; APPLICANT: ADLER, JON
; APPLICANT: XU, HONG
; APPLICANT: ECHEVERRI, FERNANDO
; TITLE OF INVENTION: TIR HETERO-OLIGOMERIC TASTE RECEPTORS AND CELL LINES
; TITLE OF INVENTION: THAT EXPRESS SAID RECEPTORS AND USE THEREOF FOR
; FILE OF INVENTION: IDENTIFICATION OF TASTE COMPOUNDS
; FILE REFERENCE: 078003-0291566
; CURRENT APPLICATION NUMBER: US/10/725,475
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/300,434
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/304,749
; PRIOR FILING DATE: 2001-07-13

; PRIOR APPLICATION NUMBER: 60/310,493
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/331,771
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/339,472
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/372,090
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: 60/374,143
; PRIOR FILING DATE: 2002-04-22
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 840
; TYPE: PRT
; ORGANISM: Rattus sp.

US-10-725-475-16

Query Match 100.0%; Score 4485; DB 9; Length 840;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 840; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLFWAAHLLLSLQVYCWAFSCQRTESSPGSLPGDFFLLAGLFSLHGDCLQVRHRLPVT 60
DB 1 MLFWAAHLLLSLQVYCWAFSCQRTESSPGSLPGDFFLLAGLFSLHGDCLQVRHRLPVT 60
QY 61 CORPDSFNGHGYHLFOAMRFTVEEINSSALLPNITLGYELVDVCSANVTATLRLVAL 120
DB 61 CORPDSFNGHGYHLFOAMRFTVEEINSSALLPNITLGYELVDVCSANVTATLRLVAL 120
QY 121 QGPRHIEIQKDLRNHSSKVAFIPGPDNDTHAVTTAALGPFLLMPLVSVYEAASSVLSAKRK 180
DB 121 QGPRHIEIQKDLRNHSSKVAFIPGPDNDTHAVTTAALGPFLLMPLVSVYEAASSVLSAKRK 180
QY 181 PFSFLRTVPSDRHQVEVMVQLQSGFWWISLIGSYGDIYGVQALBELAVPRGICVAF 240
DB 181 PFSFLRTVPSDRHQVEVMVQLQSGFWWISLIGSYGDIYGVQALBELAVPRGICVAF 240
QY 241 KDIVPFSARVGDPRMQSMQHLAQARTTVVVVFSNRHLARVFRSVVLANTLTKGVWASE 300
DB 241 KDIVPFSARVGDPRMQSMQHLAQARTTVVVVFSNRHLARVFRSVVLANTLTKGVWASE 300
QY 301 DWAISTYITSVTGIQIGITVLGVAVQOQVPGKKEFEESYVRAVTAAPSACPEGSWCSTN 360
DB 301 DWAISTYITSVTGIQIGITVLGVAVQOQVPGKKEFEESYVRAVTAAPSACPEGSWCSTN 360
QY 361 QLCRECHTFTTRNMPTLGAFAFSAAYRVYEAHVAVAGHLQLLGCTSEICSRGPVYPWOL 420
DB 361 QLCRECHTFTTRNMPTLGAFAFSAAYRVYEAHVAVAGHLQLLGCTSEICSRGPVYPWOL 420
QY 421 LQOIYKVNFLHENTVAFDDNGDTLGYDDI IAWDNMGPEWTTEIIGSASLSPVHLDINKT 480
DB 421 LQOIYKVNFLHENTVAFDDNGDTLGYDDI IAWDNMGPEWTTEIIGSASLSPVHLDINKT 480
QY 481 KIOWHGKNNQVPSVCTTDCLAGHRVWVSHHCCFECVPCBAGTFLNMSLHIQPCGCT 540
DB 481 KIOWHGKNNQVPSVCTTDCLAGHRVWVSHHCCFECVPCBAGTFLNMSLHIQPCGCT 540
QY 541 EEWAPKESITTCPRPTVEFLAWHEPISLVLIANTLHLLVGTAGLFAWHFTPVVRSAG 600
DB 541 EEWAPKESITTCPRPTVEFLAWHEPISLVLIANTLHLLVGTAGLFAWHFTPVVRSAG 600
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DB 661 FSTKVPTFTRTWAQNHGAGLFVIVSSTVHLLCLTLVWMTTPRPREYQRPFLHILECT 720
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DB 721 EYNSVGFLLAFTHNILLSTSTFVCSYLKGLPENYNEAKCVTFSLNLFVSWIAPFTMAS 780

GenCore version 5.1.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 14:33:28 ; Search time 30.1326 Seconds
(without alignments)
2310.222 Million cell updates/sec

Title: US-09-361-652-2
Perfect score: 4504
Sequence: 1 MLFWAHLHLSLQAVAYCW.....NNTHEFQASIQDYTRCGTT 842

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/1aa/5 COMB.pep.*
- 2: /cgn2_6/prodata/1/1aa/6 COMB.pep.*
- 3: /cgn2_6/prodata/1/1aa/H COMB.pep.*
- 4: /cgn2_6/prodata/1/1aa/ECTUS COMB.pep.*
- 5: /cgn2_6/prodata/1/1aa/RE COMB.pep.*
- 6: /cgn2_6/prodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1440.5	32.0	839	2	US-09-897-427A-4
3	1404	31.2	843	2	US-09-361-631-1
4	1400	31.1	843	2	US-09-361-631-2
5	1188.5	26.4	852	2	US-09-897-427A-6
6	1167.5	25.9	1059	2	US-09-334-513-2
7	1153	25.6	1078	1	US-08-485-588-7
8	1153	25.6	1078	1	US-08-484-565-7
9	1153	25.6	1078	1	US-08-480-751-7
10	1153	25.6	1078	1	US-08-943-986-7
11	1153	25.6	1078	2	US-08-353-784-7
12	1153	25.6	1078	2	US-08-484-719B-7
13	1153	25.6	1078	2	US-08-484-159-7
14	1147.5	25.5	1085	1	US-08-485-588-5
15	1147.5	25.5	1085	1	US-08-484-565-5
16	1147.5	25.5	1085	1	US-08-480-751-5
17	1147.5	25.5	1085	1	US-08-943-986-5
18	1147.5	25.5	1085	2	US-08-353-784-5
19	1147.5	25.5	1085	2	US-08-484-719B-5
20	1147.5	25.5	1085	2	US-08-484-159-5
21	1141	25.3	1088	1	US-08-485-588-6
22	1141	25.3	1088	1	US-08-484-565-6
23	1141	25.3	1088	1	US-08-480-751-6
24	1141	25.3	1088	1	US-08-943-986-6
25	1141	25.3	1088	2	US-08-353-784-6
26	1141	25.3	1088	2	US-08-484-719B-6
27	1141	25.3	1088	2	US-08-484-159-6

28	1138	25.3	1078	2	US-10-125-772-28	Sequence 28, Appl
29	1136.5	25.2	1079	1	US-08-485-588-8	Sequence 8, Appl
30	1136.5	25.2	1079	1	US-08-484-565-8	Sequence 8, Appl
31	1136.5	25.2	1079	1	US-08-480-751-8	Sequence 8, Appl
32	1136.5	25.2	1079	1	US-08-943-986-8	Sequence 8, Appl
33	1136.5	25.2	1079	2	US-08-353-784-8	Sequence 8, Appl
34	1136.5	25.2	1079	2	US-08-484-719B-8	Sequence 8, Appl
35	1136.5	25.2	1079	2	US-08-484-159-8	Sequence 8, Appl
36	1134.5	25.2	1027	2	US-09-162-021B-2	Sequence 2, Appl
37	1134.5	25.2	1027	2	US-10-268-051-8	Sequence 2, Appl
38	1134.5	25.2	1027	2	US-10-125-772-2	Sequence 2, Appl
39	1127	25.0	669	2	US-09-361-631-7	Sequence 7, Appl
40	1101.5	24.5	941	2	US-10-125-772-8	Sequence 8, Appl
41	1101.5	24.5	941	2	US-10-125-772-10	Sequence 10, Appl
42	1078.5	23.9	850	2	US-10-125-772-12	Sequence 12, Appl
43	1043	23.2	1219	1	US-08-687-289A-6	Sequence 6, Appl
44	1043	23.2	1219	2	US-09-435-897-6	Sequence 6, Appl
45	1030	22.9	851	2	US-09-619-353-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-897-427A-2
; Sequence 2, Application US/09897427A
; Patent No. 6955887
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; APPLICANT: LI, XIADONG
; APPLICANT: STAZEMSKI, LENA
; APPLICANT: XU, HONG
; APPLICANT: EHEVERRI, FERNANDO
; TITLE OF INVENTION: T1R HETERO-OLIGOMERIC TASTE RECEPTORS
; FILE REFERENCE: 078003-0282558
; CURRENT APPLICATION NUMBER: US/09/897,427A
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 841
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-427A-2

Query Match		74.3%	Score 3348.5;	DB 2;	Length 841;
Best Local Similarity		73.5%	Pred. No. 2.7e-309;		
Matches 619;		Conservative	87;	Mismatches 135;	Indels 1; Gaps 1;
QY	1	MLFWAHLHLSLQAVAYCWAFSCORTESSPGFLPGDFLLAGLPSLHADCLQVRHPLV	60		
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QY	61	TCSDRSDSNGHYHLFOAMRTTVEINNSTALLNITGLYLYDYVCSSESSVYATLRVP	120		
DB	60	TLCDSRCSFNGHYHLFOAMRLGVEINNSTALLNITGLYQLYDYVCSDSANVYATLRVL	119		
QY	121	AQQTGTHLWMQDLRNHSSKVVALLIGPDNTDRAVTTAALLSPFLMPLVSYEASSVILSGK	180		
DB	120	SLFGQHILSLQDGLLHYSPVLAVIGPDSTNRAVTTAALLSPFLVPMVSYAASSETLSVK	179		
QY	181	RKPPSPFLRTPSDKYQVEVIVRLLOSFGVWVWISLVGSGYDYGQGLGVQALBELATPRGICV	240		
DB	180	RQYPSFLRTPNDKYQVETWVLLLOKFGMTWISLVGSSDDYDYGQGLVQALENQATGQICV	239		
QY	241	AFKDVVPLSAQAGDPQMOMRLARPTVVVPSNRHLAGVFFSVVLNLTGKVWIA	300		
DB	240	AFKDIIMPFAQVQDERMOCIMRHLAQAGATVVVVFSSRLQARVFFSVVLNLTGKVWIA	299		
QY	301	SEDMALSTVITNVPQIGIGTGLGVAIQOQVPGKLFEEESYVQAVMGAPRTCPGSGWC	360		
DB	300	SEANLSRHTITGVPGIQRIGWLVGVAIQKRVPLKAFENYARADKAPRCPCHKSGWCS	359		

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DB 360 SNOLCRECOFAWHTMPKLFKAFMSAYNAYAVAVAGHLLHLLGCTSGTCARGPVYPW 419
QY 421 QLLQOIKYKYNFLHKKTKTAFDDKDPGLGYDIIAMDWNGPEWTFEIVGSASLSPVHLDTN 480
DB 420 QLEQIKHVKHFLHKKTKTAFDDKDPGLGYDIIAMDWNGPEWTFEIVGSASLSPVHLDTN 479
QY 481 KTKIQHKGKNNQVPVSVCTRDCLGHRHLMVSHHCCFECMPCCEAGTFLNTSELHCTQPC 540
DB 480 ETKIQHKGKNNQVPVSVCTRDCLGHRHLMVSHHCCFECMPCCEAGTFLNTSELHCTQPC 539
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DB 540 GKEEWAPESSACFSSTVEFLGHEPISLVLAANTLIIALLIGTAGLPAWLHPTVVR 599
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DB 600 AGGRCLFMLGSLVAGSCSLYSPFGKPTVPACILRQPLFSLGFAIFLSCLTIRSFQVLII 659
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DB 660 KPESTKVPFYTNAQNHGAGIFVIVSVTHLFLCLTULWAMTTPRTBYQRPPLHVL 719
QY 721 CTEVNSVGLVAFANHLLISITFVCSYLGKLPENYNEAKCVTFSLHLLHFSWIAFTM 780
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DB 840 ST 841

RESULT 2
US-09-897-427A-4
; Sequence 4, Application US/09897427A
; Patent No. 6955887
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; APPLICANT: LI, XIADONG
; APPLICANT: STAZEWSKI, LENA
; APPLICANT: XU, HONG
; APPLICANT: EHEVERRI, FERNANDO
; TITLE OF INVENTION: T1R HETERO-OLIGOMERIC TASTE RECEPTORS
; FILE REFERENCE: 078003-0282558
; CURRENT APPLICATION NUMBER: US/09/897,427A
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-427A-4

Query Match 32.0%; Score 1440.5; DB 2; Length 839;
Best Local Similarity 39.8%; Pred. No. 1.2e-127;
Matches 329; Conservative 121; Mismatches 341; Indels 35; Gaps 15;

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QY 91 TALLPNITIGELYDYDVCSSSNVYATLRVPAQOGTGHLEMQORDLRNHSKVALIGPDYT 150
DB 86 SLLPGVLLGYEYVDVYCSNNQPVLYFLAHE-DNLLPIQEDYSYISRWAVIGPDNS 144
QY 151 DRAVTTAALLSPMLVSYEASVILSGRKPFPFLRTIPSDKYQVEIVIRLLOSGFW 210
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DB 205 WIIVLVSDTYGRDNGQLGERVARDDICIAPOETLPTLQPNQNTSBEROKLVITVDKL 264
QY 265 ARARTTVVVVNRHLAGVFFRSVVLNLTGKVTIASDWAISTYITNVPGIQIGITVLG 324
DB 265 QOSTARVVVVVSPDLTLHFNEVLNQFTGAVWIASDWAIDPVLHNLTELHGLGTFLG 324
QY 325 VAIQORQVPLGKFEESYVQAVMGAPRTCPGEGMCGTQOLCRECHAPTNNPGLGAFMS 384
DB 325 ITIQSVPIPGSEFPEMGPOA--GPPPLSRTSQSTCQECDCNCLNATLSFNTILRLSGE 382
QY 385 SAANYVYAVAVAGHLLHLLGCTSGTCARGPVYPWQLLQIYKYNFLHKKTKTAFDDKG 444
DB 383 RVYSVYAVAVAGHLLHLLGCTSGTCARGPVYPWQLLQIYKYNFLHKKTKTAFDDKG 442
QY 445 DPLGYDIIAMDWNGPEWTFEIVGSASLSPVHLDT--NKTQIOWHKGKNNQVPVSVCTRDCL 503
DB 443 DVALHLEIVQWQDRSQNPFSQV--ASYVPLQRLQKNIQDISWHTVNTIPMSMCKRCQ 500
QY 504 EGHRLVMGSHHCCFECMPCBAGTFLN--TSELHTCQPCGTBEWAPEGSACFSRTVEFLG 562
DB 501 SQQKKKPVGIIHVCCPECIDCLPGLTFLNHTDEYEQACPNNEWSYQSETSCFKRLQVLE 560
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RESULT 3
US-09-361-631-1
; Sequence 1, Application US/09361631
; Patent No. 6383778
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Lindemeier, Juergen
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor
; TITLE OF INVENTION: Involved in Sensory Transduction
; FILE REFERENCE: 02307E-088720US
; CURRENT APPLICATION NUMBER: US/09/361,631
; CURRENT FILING DATE: 1999-07-27
; EARLIER APPLICATION NUMBER: US 60/095,464
; EARLIER FILING DATE: 1998-07-28
; EARLIER APPLICATION NUMBER: US 60/112,747
; EARLIER FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 843
; TYPE: PRT
; ORGANISM: Rattus sp.
; FEATURE:
; OTHER INFORMATION: rat G-protein coupled receptor (GPCR) B4 amino
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 14:52:34 ; Search time 101.013 Seconds
(without alignments)
3482.855 Million cell updates/sec

Title: US-09-361-652-2

Perfect score: 4504

Sequence: 1 MLFWAHLHLLSLQAVAYCW.....NNTSHFOASIQDYTRRCOTT 842

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:*

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- 2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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6	4479	99.4	842	4	US-10-436-715-35
7	4479	99.4	842	4	US-10-436-715-67
8	4455	98.9	842	4	US-10-436-715-68
9	4100	91.0	840	3	US-09-361-652-1
10	4100	91.0	840	3	US-09-361-652-1
11	4100	91.0	840	4	US-10-246-785-3
12	4100	91.0	840	4	US-10-190-417-1
13	4100	91.0	840	4	US-10-159-339-12
14	4100	91.0	840	4	US-10-179-373-16
15	4100	91.0	840	4	US-10-436-715-39
16	4100	91.0	840	4	US-10-436-715-69
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18	4100	91.0	840	4	US-10-725-489-16
19	4100	91.0	840	4	US-10-725-080A-16
20	4100	91.0	840	4	US-10-725-472A-16
21	4100	91.0	840	5	US-10-725-418-16
22	4100	91.0	840	5	US-10-679-102-1
23	3656.5	81.2	1138	4	US-10-261-482-4
24	3349.5	74.4	841	4	US-10-188-186-2
25	3348.5	74.3	841	3	US-09-819-946-2
26	3348.5	74.3	841	3	US-09-897-427A-2
27	3348.5	74.3	841	3	US-09-799-629-17

28 3348.5 74.3 841 4 US-10-035-045-17 Sequence 17, Appl
29 3348.5 74.3 841 4 US-10-417-27 Sequence 27, Appl
30 3348.5 74.3 841 4 US-10-179-373-5 Sequence 5, Appl
31 3348.5 74.3 841 4 US-10-311-196-3 Sequence 3, Appl
32 3348.5 74.3 841 4 US-10-725-081-17 Sequence 17, Appl
33 3348.5 74.3 841 4 US-10-724-223-17 Sequence 5, Appl
34 3348.5 74.3 841 4 US-10-725-103-5 Sequence 5, Appl
35 3348.5 74.3 841 4 US-10-725-489-5 Sequence 5, Appl
36 3348.5 74.3 841 4 US-10-724-222-17 Sequence 17, Appl
37 3348.5 74.3 841 4 US-10-725-472A-5 Sequence 5, Appl
38 3348.5 74.3 841 4 US-10-725-276-17 Sequence 17, Appl
39 3348.5 74.3 841 4 US-10-770-127-197 Sequence 157, App
40 3348.5 74.3 841 5 US-10-726-568-17 Sequence 17, Appl
41 3348.5 74.3 841 5 US-10-725-284-17 Sequence 2, Appl
42 3348.5 74.3 841 5 US-10-885-493-2 Sequence 5, Appl
43 3348.5 74.3 841 5 US-10-725-418-5 Sequence 27, Appl
44 3348.5 74.3 841 5 US-10-679-102-27 Sequence 27, Appl
45 3348.5 74.3 841 5 US-10-679-102-27 Sequence 27, Appl

ALIGNMENTS

RESULT 1

US-09-361-652-2
; Sequence 2, Application US/09361652
; Publication No. US20030036630A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Lindemeier, Juerger
; APPLICANT: Ryba, Nick
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor
; FILE REFERENCE: 02307E-088610US
; CURRENT APPLICATION NUMBER: US/09/361.652
; CURRENT FILING DATE: 1999-07-27
; EARLIER APPLICATION NUMBER: US 60/094,465
; EARLIER FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 842
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: mouse G-protein coupled receptor B3 (GPCR-B3)
US-09-361-652-2

Query Match 100.0%; Score 4504; DB 3; Length 842;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 842; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MLFWAHLHLLSLQAVAYCWAFSCQRTSSPGFSLPGDPLAGLFSHADCLQVRHPLV 60
QY 61 TSCDRSDSFNGHGHVLFQAMRFTVEEINNSTALLPNTLTGLYELVDVCSSENNVATLRVP 120
DB 61 TSCDRSDSFNGHGHVLFQAMRFTVEEINNSTALLPNTLTGLYELVDVCSSENNVATLRVP 120
QY 121 AQQGTGHELMORDLRNHSSKVVALIGPDNTHAVTTAALLSPFLMPLVSEASSVILSGK 180
DB 121 AQQGTGHELMORDLRNHSSKVVALIGPDNTHAVTTAALLSPFLMPLVSEASSVILSGK 180
QY 181 RKFPSTLTIPSDKYQVEVIRLLQSGFWVWISLVGSDYDYGQGLGVALBELATPRGICV 240
DB 181 RKFPSTLTIPSDKYQVEVIRLLQSGFWVWISLVGSDYDYGQGLGVALBELATPRGICV 240
QY 241 AFKDVVPLSAQAQDPFRMQLRLARATTVVVVPSNHLGAVFPRSVLNLTKGWIA 300

Db 241 AFKDVVPLSAQAQDPRMQRMLRLARATTVVVVFSNRHLAGVFFRSVVLANTLTKVWIA 300
Qy 301 SEDWASTYITNVPQIGITGVLGVAIQORQVGLKEFEESYVOAVMGAPRTCPGSMCG 360
Db 301 SEDWASTYITNVPQIGITGVLGVAIQORQVGLKEFEESYVOAVMGAPRTCPGSMCG 360
Qy 361 TNOLCRECHAFPTWNPDELGAFAFMSAAYNYEAVYAVAGHLHQLLCTGTCARGPVYPM 420
Db 361 TNOLCRECHAFPTWNPDELGAFAFMSAAYNYEAVYAVAGHLHQLLCTGTCARGPVYPM 420
Qy 421 QLLQOIYKYNFLHKKTVAFDDKGPLGYDYDIIAOWNGPEWTFEVIQSASLSPVHLIN 480
Db 421 QLLQOIYKYNFLHKKTVAFDDKGPLGYDYDIIAOWNGPEWTFEVIQSASLSPVHLIN 480
Qy 481 KTKIOWHGKNNQVPSVCTRDCLGHHRLVMGSHHCCFECMPCCEAGTFLNTSELHTCQPC 540
Db 481 KTKIOWHGKNNQVPSVCTRDCLGHHRLVMGSHHCCFECMPCCEAGTFLNTSELHTCQPC 540
Qy 541 GTEWAPGSSACFSRTVEFLGWHEPIISLVLLAANTLLLLIGTAGLPAWRLHTPVVRS 600
Db 541 GTEWAPGSSACFSRTVEFLGWHEPIISLVLLAANTLLLLIGTAGLPAWRLHTPVVRS 600
Qy 601 AGRLCFLMLGSLVAGSCSLYSFFGKPTVPACLLRQPLFLSLGFAIFLSCLTIRSFQVLI 660
Db 601 AGRLCFLMLGSLVAGSCSLYSFFGKPTVPACLLRQPLFLSLGFAIFLSCLTIRSFQVLI 660
Qy 661 FKSTKVPPTYHTWAQNHGAGIFVIVSSTVHLFLCLTLWAMWTPRTREYQRPVHLVILE 720
Db 661 FKSTKVPPTYHTWAQNHGAGIFVIVSSTVHLFLCLTLWAMWTPRTREYQRPVHLVILE 720
Qy 721 CTEVNSVGLFVAFVHNILLISITFVCSYLKELPENYNEAKCVTFSLHLHFVSWIAFFTM 780
Db 721 CTEVNSVGLFVAFVHNILLISITFVCSYLKELPENYNEAKCVTFSLHLHFVSWIAFFTM 780
Qy 781 SSIYQGSYLPAVNVLAGLTLGGFGSGYFLPKCVILCRPELNTEHFQASIQDYTRRCG 840
Db 781 SSIYQGSYLPAVNVLAGLTLGGFGSGYFLPKCVILCRPELNTEHFQASIQDYTRRCG 840
Qy 841 TT 842
Db 841 TT 842

RESULT 2

US-09-927-315-2
; Sequence 2, Application US/09927315
; Publication No. US20030040045A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Ryba, Nicholas J.P.
; APPLICANT: Nelson, Greg
; APPLICANT: Hoon, Mark A.
; APPLICANT: Chandrashekar, Jayaram
; APPLICANT: Zhang, Yifeng
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Mammalian Sweet Taste Receptors
; FILE REFERENCE: 02307E-120110US
; CURRENT APPLICATION NUMBER: US/09/927,315
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/302,898
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 842
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: mouse Tir1 sweet taste receptor
US-09-927-315-2

Query Match 100.0%; Score 4504; DB 3; Length 842;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 842; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLFMAAHLILLSQLAVAYCWFAPSCQRTSSSPGFSPLPGDFLLAGLSLHADCLQVHRPLV 60
Db 1 MLFMAAHLILLSQLAVAYCWFAPSCQRTSSSPGFSPLPGDFLLAGLSLHADCLQVHRPLV 60
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Db 61 TSCDRSDSPNGHGYHLFOAMRTVEIINNSTALLNITLGVELYDVCSESSNYATLRVP 120
Qy 121 AOQGTGHEMQORDLNHSSKVALLGPONTDHAVTTAALLSPFLMPLVSYEASSVILSK 180
Db 121 AOQGTGHEMQORDLNHSSKVALLGPONTDHAVTTAALLSPFLMPLVSYEASSVILSK 180
Qy 181 RKPPSFLRTIPSDKYQVEIVRLQSGFVWISLVGSYDYGQQLGVQALAEELATPRGICV 240
Db 181 RKPPSFLRTIPSDKYQVEIVRLQSGFVWISLVGSYDYGQQLGVQALAEELATPRGICV 240
Qy 241 AFKDVVPLSAQAQDPRMQRMLRLARATTVVVVFSNRHLAGVFFRSVVLANTLTKVWIA 300
Db 241 AFKDVVPLSAQAQDPRMQRMLRLARATTVVVVFSNRHLAGVFFRSVVLANTLTKVWIA 300
Qy 301 SEDWASTYITNVPQIGITGVLGVAIQORQVGLKEFEESYVOAVMGAPRTCPGSMCG 360
Db 301 SEDWASTYITNVPQIGITGVLGVAIQORQVGLKEFEESYVOAVMGAPRTCPGSMCG 360
Qy 361 TNOLCRECHAFPTWNPDELGAFAFMSAAYNYEAVYAVAGHLHQLLCTGTCARGPVYPM 420
Db 361 TNOLCRECHAFPTWNPDELGAFAFMSAAYNYEAVYAVAGHLHQLLCTGTCARGPVYPM 420
Qy 421 QLLQOIYKYNFLHKKTVAFDDKGPLGYDYDIIAOWNGPEWTFEVIQSASLSPVHLIN 480
Db 421 QLLQOIYKYNFLHKKTVAFDDKGPLGYDYDIIAOWNGPEWTFEVIQSASLSPVHLIN 480
Qy 481 KTKIOWHGKNNQVPSVCTRDCLGHHRLVMGSHHCCFECMPCCEAGTFLNTSELHTCQPC 540
Db 481 KTKIOWHGKNNQVPSVCTRDCLGHHRLVMGSHHCCFECMPCCEAGTFLNTSELHTCQPC 540
Qy 541 GTEWAPGSSACFSRTVEFLGWHEPIISLVLLAANTLLLLIGTAGLPAWRLHTPVVRS 600
Db 541 GTEWAPGSSACFSRTVEFLGWHEPIISLVLLAANTLLLLIGTAGLPAWRLHTPVVRS 600
Qy 601 AGRLCFLMLGSLVAGSCSLYSFFGKPTVPACLLRQPLFLSLGFAIFLSCLTIRSFQVLI 660
Db 601 AGRLCFLMLGSLVAGSCSLYSFFGKPTVPACLLRQPLFLSLGFAIFLSCLTIRSFQVLI 660
Qy 661 FKSTKVPPTYHTWAQNHGAGIFVIVSSTVHLFLCLTLWAMWTPRTREYQRPVHLVILE 720
Db 661 FKSTKVPPTYHTWAQNHGAGIFVIVSSTVHLFLCLTLWAMWTPRTREYQRPVHLVILE 720
Qy 721 CTEVNSVGLFVAFVHNILLISITFVCSYLKELPENYNEAKCVTFSLHLHFVSWIAFFTM 780
Db 721 CTEVNSVGLFVAFVHNILLISITFVCSYLKELPENYNEAKCVTFSLHLHFVSWIAFFTM 780
Qy 781 SSIYQGSYLPAVNVLAGLTLGGFGSGYFLPKCVILCRPELNTEHFQASIQDYTRRCG 840
Db 781 SSIYQGSYLPAVNVLAGLTLGGFGSGYFLPKCVILCRPELNTEHFQASIQDYTRRCG 840
Qy 841 TT 842
Db 841 TT 842

RESULT 3

US-10-246-785-2
; Sequence 2, Application US/10246785
; Publication No. US20030148448A1
; GENERAL INFORMATION:
; APPLICANT: IRM, LLC
; APPLICANT: The Scripps Research Institute

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 14:54:39 ; Search time 16.0935 Seconds
(without alignments)

2421.578 Million cell updates/sec

Title: US-09-361-652-2

Perfect score: 4504

Sequence: 1 MLFWAHLHLLSLQAVAYCW.....NNTHEFQASIQDYTRCGTT 842

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:

1: /SIDSS5/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /SIDSS5/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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11: /SIDSS5/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
12: /SIDSS5/ptodata/2/pubpaa/US11_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4504	100.0	842	9	US-10-645-441-2
2	4100	91.0	840	9	US-10-645-441-1
3	4100	91.0	840	9	US-10-725-475-16
4	3348.5	74.3	841	9	US-10-725-475-5
5	3348.5	74.3	841	11	US-11-050-804-2
6	3104.5	68.9	777	9	US-10-645-441-3
7	1440.5	32.0	839	9	US-10-725-475-6
8	1440.5	32.0	839	11	US-11-050-804-4
9	1434	31.8	838	9	US-10-645-441-9
10	1404	31.2	843	9	US-10-645-441-7
11	1404	31.2	843	9	US-10-725-475-17
12	1400	31.1	843	9	US-10-645-441-8
13	1191.5	26.4	852	9	US-10-725-475-7
14	1188.5	26.4	852	9	US-10-645-441-15
15	1188.5	26.4	852	11	US-11-050-804-6
16	1178	26.2	858	9	US-10-645-441-25
17	1178	26.2	858	9	US-10-725-475-4
18	1167.5	25.9	858	9	US-10-645-441-18
19	1163.5	25.8	858	9	US-10-645-441-20
20	1159.5	25.7	858	9	US-10-645-441-23
21	1145	25.4	867	9	US-10-725-475-19

22	1077	23.9	928	9	US-10-841-129-4	Sequence 4, Appli
23	1051	23.3	928	9	US-10-841-129-6	Sequence 6, Appli
24	1012	22.5	926	9	US-10-841-129-2	Sequence 2, Appli
25	737	16.4	1199	9	US-10-922-166-15	Sequence 15, Appl
26	734	16.3	845	9	US-10-725-475-18	Sequence 18, Appl
27	713	15.8	879	9	US-10-877-346-17	Sequence 17, Appl
28	708	15.7	879	9	US-10-877-346-53	Sequence 53, Appl
29	707	15.7	879	9	US-10-877-346-52	Sequence 54, Appl
30	701	15.6	879	9	US-10-877-346-52	Sequence 52, Appl
31	680	15.1	865	11	US-11-094-519A-41	Sequence 41, Appl
32	470.5	10.4	242	9	US-10-725-475-13	Sequence 13, Appl
33	446.5	9.9	497	9	US-10-918-857-8	Sequence 8, Appli
34	446.5	9.9	576	9	US-10-922-166-2	Sequence 2, Appli
35	446.5	9.9	790	9	US-10-918-857-6	Sequence 6, Appli
36	446.5	9.9	790	9	US-10-922-166-20	Sequence 15, Appl
37	378	8.4	236	9	US-10-725-475-15	Sequence 4, Appli
38	374	8.3	425	9	US-10-918-857-4	Sequence 2, Appli
39	374	8.3	718	9	US-10-918-857-2	Sequence 85, Appl
40	370.5	8.2	256	9	US-10-877-346-85	Sequence 14, Appl
41	336.5	7.5	165	9	US-10-725-475-14	Sequence 12, Appl
42	310.5	6.9	137	9	US-10-725-475-12	Sequence 84, Appl
43	286	6.3	402	9	US-10-877-346-84	Sequence 40, Appl
44	193	4.3	844	11	US-11-127-877-40	Sequence 2, Appli
45	150.5	3.3	885	9	US-10-912-971-2	

ALIGNMENTS

RESULT 1

US-10-645-441-2
; Sequence 2, Application US/10645441
; Publication No. US20050260599A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Ryba, Nicholas J.P.
; APPLICANT: Nelson, Greg
; APPLICANT: Hoon, Mark A.
; APPLICANT: Chandrasekar, Jayaram
; APPLICANT: Zhang, Yifeng
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Mammalian Sweet Taste Receptors
; FILE REFERENCE: 023078-120110US
; CURRENT APPLICATION NUMBER: US/10/645,441
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: US/09/927,315
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/302,898
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.1
; LENGTH: 842
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: mouse Tir1 sweet taste receptor
US-10-645-441-2

Query Match 100.0%; Score 4504; DB 9; Length 842;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 842; Conservative. 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MLFWAHLHLLSLQAVAYCWAFSCQRTSSPGSLPGDFLLAGLFLSLHACDLQVRHPLV 60

Qy 61 TSCDRSDSFNGHGHYLFQAMRFTVEEINNSTALLPNITLGVLYDYVCSSESNVYATLRVP 120

Db 61 TSCDRSDSFNGHGHYLFQAMRFTVEEINNSTALLPNITLGVLYDYVCSSESNVYATLRVP 120

121 AOGTGHLEMDRLNRHSSKVALIGPDNTDHAIVTTAAALLSPFLPLVSYEASSVILSK 180
121 AOGTGHLEMDRLNRHSSKVALIGPDNTDHAIVTTAAALLSPFLPLVSYEASSVILSK 180
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181 RFPSPFLRTIPSDKYQVEVIVRLQLQSGFWWISLVGSYDYGQVQALAEELATPRGICV 240
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421 QLLQQIYKVNFLHKKTVAFDDKGDPLGYDIIANDWNGPEWTFEIVGSASLSPVHLDIN 480
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661 FKPFSTKVPFTYHTWAQNHGAGIFVIVSVSTVHLPLCLTTLAMWTPRTREYQRPPLVILE 720
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721 CTEVNSVGLVPAFAHNILISITFVCSYLGKELPENYNEAKCVTFSLLLHFVSWIAFFTM 780
721 CTEVNSVGLVPAFAHNILISITFVCSYLGKELPENYNEAKCVTFSLLLHFVSWIAFFTM 780
781 SSIYQGSYLPVAVNLVAGLATLSGGFSGYFLPKCYVILCRPELNTHEFQASIQDYTRRCG 840
781 SSIYQGSYLPVAVNLVAGLATLSGGFSGYFLPKCYVILCRPELNTHEFQASIQDYTRRCG 840
841 TT 842
841 TT 842

RESULT 2

US-10-645-441-1

Sequence 1, Application US/10645441

Publication No. US20050260599A1

GENERAL INFORMATION:

APPLICANT: Zuker, Charles S.

APPLICANT: Ryba, Nicholas J.P.

APPLICANT: Nelson, Greg

APPLICANT: Hoon, Mark A.

APPLICANT: Chandrashekar, Jayaram

APPLICANT: Zhang, Yifeng

APPLICANT: The Regents of the University of California

APPLICANT: The Government of the United States of America

APPLICANT: as represented by the Secretary of the

APPLICANT: Department of Health and Human Services

TITLE OF INVENTION: Mammalian Sweet Taste Receptors

FILE REFERENCE: 023078-120110US

CURRENT APPLICATION NUMBER: US/10/645,441

CURRENT FILING DATE: 2003-08-20

; PRIOR APPLICATION NUMBER: US/09/927,315

; PRIOR FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: US 60/302,898

; PRIOR FILING DATE: 2001-07-03

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 840

; TYPE: PRT

; ORGANISM: Rattus sp.

; FEATURE:

; OTHER INFORMATION: rat T1R1 sweet taste receptor

US-10-645-441-1

Query Match 91.0%; Score 4100; DB 9; Length 840;

Best Local Similarity 89.9%; Fred. No. 0;

Matches 757; Conservative 35; Mismatches 48; Indels 2; Gaps 1;

QY 1 MLFWAAHLLLSLQLAVAYCWAFCQRTSSSPGSLPGDFLLAGLFSLHADCLQVRRPLV 60

DB 1 MLFWAAHLLLSLQL--VVCWAFSCQRTSSSPGSLPGDFLLAGLFSLHADCLQVRRPLV 58

QY 61 TSCDSRDSFNGHYHLFOAMRPTVEEINNSTALLNITILGYELYDYVCSSESNVYATLRVP 120

DB 59 TSCDRPDSFNGHYHLFOAMRPTVEEINNSTALLNITILGYELYDYVCSSESNVYATLRV 118

QY 121 AOOGTGHLEMDRLNRHSSKVALIGPDNTDHAIVTTAAALLSPFLPLVSYEASSVILSK 180

DB 119 ALQOGPRHEIOKDLNRHSSKVVAFIGPDNTDHAIVTTAAALLSPFLPLVSYEASSVILSK 178

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DB 179 RKFPFLRTIPSDKYQVEVIVRLQLQSGFWWISLVGSYDYGQVQALAEELATPRGICV 238

QY 241 AFKDVVPLSAQAGDPRMQRMLRLARARTVVVVFSNRHLGAVFFRSVVLANLTGKWITA 300

DB 239 AFKDVVPLSAQAGDPRMQRMLRLARARTVVVVFSNRHLGAVFFRSVVLANLTGKWITA 298

QY 301 SEDMAISTITNVPGIQIGTGLGVAVIQORQVPLKEPEESYVQAVMGAPRTCPGSGWC 360

DB 299 SEDMAISTITNVPGIQIGTGLGVAVIQORQVPLKEPEESYVQAVMGAPRTCPGSGWC 358

QY 361 TNLQCRECHAFPTWNNPELGAFSMAAANNVYEAIVAAHGLHQLLCTSGTCARGPVYFW 420

DB 359 TNLQCRECHAFPTWNNPELGAFSMAAANNVYEAIVAAHGLHQLLCTSGTCARGPVYFW 418

QY 421 QLLQQIYKVNFLHKKTVAFDDKGDPLGYDIIANDWNGPEWTFEIVGSASLSPVHLDIN 480

DB 419 QLLQQIYKVNFLHKKTVAFDDKGDPLGYDIIANDWNGPEWTFEIVGSASLSPVHLDIN 478

QY 481 KTKIOWHGKNNQVPVSVCTRDCLGHHRLVMSGHCCFECMPCCEAGTFLNTSELHTCQPC 540

DB 479 KTKIOWHGKNNQVPVSVCTRDCLGHHRLVMSGHCCFECMPCCEAGTFLNTSELHTCQPC 538

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DB 539 GTEEWAPESSACFSRTVEFLGWHEPISLVLLAANTLLLLLLIGTAGLFAWRLHTPVVRS 598

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DB 599 AGGRLCFLMLGSLVAGSCSLYSPFGKPTVPACLLRQPLFSLGPAIFLCLTIRSFQLVII 658

QY 661 FKPFSTKVPFTYHTWAQNHGAGIFVIVSVSTVHLPLCLTTLAMWTPRTREYQRPPLVILE 720

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QY 781 SSIYQGSYLPVAVNLVAGLATLSGGFSGYFLPKCYVILCRPELNTHEFQASIQDYTRRCG 840

DB 779 SSIYQGSYLPVAVNLVAGLATLSGGFSGYFLPKCYVILCRPELNTHEFQASIQDYTRRCG 838

GenCore version 5.1.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 4, 2006, 14:33:28 ; Search time 27.8064 Seconds
(without alignments)
2310.222 Million cell updates/sec

Title: US-09-361-652-3
Perfect score: 4138
Sequence: 1 RSCSPNEHGYHLFQAMRLGV.....NSTEHFQSIQDYTRRCGST 777

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues
Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1288	31.1	843	2	US-09-361-631-1
3	1267.5	30.6	839	2	US-09-897-427A-4
4	1258.5	30.4	843	2	US-09-361-631-2
5	1064	25.7	669	2	US-09-361-631-7
6	1053	25.4	852	2	US-09-897-427A-6
7	1038.5	25.1	1078	1	US-08-485-588-7
8	1038.5	25.1	1078	1	US-08-484-565-7
9	1038.5	25.1	1078	1	US-08-480-751-7
10	1038.5	25.1	1078	1	US-08-943-986-7
11	1038.5	25.1	1078	2	US-08-353-784-7
12	1038.5	25.1	1078	2	US-08-484-719B-7
13	1038.5	25.1	1078	2	US-08-484-159-7
14	1038	25.1	1059	2	US-09-134-513-2
15	1026.5	24.8	1088	1	US-08-485-588-6
16	1026.5	24.8	1088	1	US-08-484-565-6
17	1026.5	24.8	1088	1	US-08-480-751-6
18	1026.5	24.8	1088	1	US-08-943-986-6
19	1026.5	24.8	1088	2	US-08-353-784-6
20	1026.5	24.8	1088	2	US-08-484-719B-6
21	1026.5	24.8	1088	2	US-08-484-159-6
22	1025.5	24.8	1079	1	US-08-485-588-8
23	1025.5	24.8	1079	1	US-08-484-565-8
24	1025.5	24.8	1079	1	US-08-480-751-8
25	1025.5	24.8	1079	1	US-08-943-986-8
26	1025.5	24.8	1079	2	US-08-353-784-8
27	1025.5	24.8	1079	2	US-08-484-719B-8

28	1025.5	24.8	1079	2	US-08-484-159-8	Sequence 8, Appl1
29	1024.5	24.8	1085	1	US-08-485-588-5	Sequence 5, Appl1
30	1024.5	24.8	1085	1	US-08-484-565-5	Sequence 5, Appl1
31	1024.5	24.8	1085	1	US-08-480-751-5	Sequence 5, Appl1
32	1024.5	24.8	1085	1	US-08-943-986-5	Sequence 5, Appl1
33	1024.5	24.8	1085	2	US-08-153-784-5	Sequence 5, Appl1
34	1024.5	24.8	1085	2	US-08-484-719B-5	Sequence 5, Appl1
35	1024.5	24.8	1085	2	US-08-484-159-5	Sequence 5, Appl1
36	1022.5	24.7	1078	2	US-10-125-772-28	Sequence 28, Appl1
37	1005.5	24.3	941	2	US-10-125-772-8	Sequence 10, Appl1
38	1005.5	24.3	941	2	US-10-125-772-10	Sequence 2, Appl1
39	1004.5	24.3	1027	2	US-10-268-051-8	Sequence 8, Appl1
40	1004.5	24.3	1027	2	US-10-125-772-2	Sequence 2, Appl1
41	984.5	23.8	1219	1	US-08-687-289A-6	Sequence 6, Appl1
42	984.5	23.8	1219	2	US-09-435-897-6	Sequence 12, Appl1
43	981.5	23.7	850	2	US-10-125-772-12	Sequence 12, Appl1
44	981.5	23.7	850	2	US-09-619-353-8	Sequence 8, Appl1
45	953.5	23.0	856	2	US-09-619-353-8	Sequence 8, Appl1

ALIGNMENTS

RESULT 1
US-09-897-427A-2
; Sequence 2, Application US/09897472A
; Patent No. 6955887
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; APPLICANT: LI, XIADONG
; APPLICANT: STAZEWSKI, LENA
; APPLICANT: XU, HONG
; APPLICANT: RHEVERRI, FERNANDO
; TITLE OF INVENTION: T1R HETERO-OLIGOMERIC TASTE RECEPTORS
; FILE REFERENCE: 078003-0282558
; CURRENT APPLICATION NUMBER: US/09/897,427A
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 841
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-427A-2

Query Match	98.2%	Score	4064.5	DB 2	Length	841
Best Local Similarity	98.5%	Pred. No.	0			
Matches	766	Conservative	5	Mismatches	6	Indels 1; Gaps 1;
QY	1	RSCSPNEHGYHLFQAMRLGV	EINNSTALLPNITLGYQLYDV	CSDSANVYATLRLVLSLPG	60	
DB	64	RSCSPNEHGYHLFQAMRLGV	EINNSTALLPNITLGYQLYDV	CSDSANVYATLRLVLSLPG	123	
QY	61	QHHEIQGLLLHSPYTPVLAV	IGPDSNTRATTAALSPPLV	-HISYAASSETLSVKRQYP	119	
DB	124	QHHEIQGLLLHSPYTPVLAV	IGPDSNTRATTAALSPPLV	MISYAASSETLSVKRQYP	183	
QY	120	SFLRTIPNDKYQVETWVLL	LQKFGTWISLVGSSDDY	QGLGVQALNQALVRGICIAFKD	179	
DB	184	SFLRTIPNDKYQVETWVLL	LQKFGTWISLVGSSDDY	QGLGVQALNQALVRGICIAFKD	243	
QY	180	IMPFSAQVGDERRMQLMR	HLAQAGATVWVVFSSRLAR	VPFESVLTNLTKGVWVASEAW	239	
DB	244	IMPFSAQVGDERRMQLMR	HLAQAGATVWVVFSSRLAR	VPFESVLTNLTKGVWVASEAW	303	
QY	240	ALSRHTGVPGIQRIQW	IGVGLVAIQKAVPGLKAP	EEYARADKEAPRCHKGSCSNQL	299	
DB	304	ALSRHTGVPGIQRIQW	IGVGLVAIQKAVPGLKAP	EEYARADKEAPRCHKGSCSNQL	363	
QY	300	CRECOAPMAHTMPKLP	KAFPMSSAYNAYRAYVA	VAHGLHQLLGCASELCSGRVYPMQLE	359	
DB	364	CRECOAPMAHTMPKLP	KAFPMSSAYNAYRAYVA	VAHGLHQLLGCASELCSGRVYPMQLE	423	

360	QIHKVHFLLHKOTVAFNDNRDPLSSYNI	IAWDNMGPKWTTFTVLGSSTWSPVQLINETKI	419
	QIHKVHFLLHKOTVAFNDNRDPLSSYNI	IAWDNMGPKWTTFTVLGSSTWSPVQLINETKI	
424	QIHKVHFLLHKOTVAFNDNRDPLSSYNI	IAWDNMGPKWTTFTVLGSSTWSPVQLINETKI	483
	QIHKVHFLLHKOTVAFNDNRDPLSSYNI	IAWDNMGPKWTTFTVLGSSTWSPVQLINETKI	
420	QWKGKNOHPKSVCSDDCL	EGHORVVTFGHCCFECPCGAGTFLNKSSELYRCOPCGTBE	479
	::		
484	QWKGKNOHPKSVCSDDCL	EGHORVVTFGHCCFECPCGAGTFLNKSDDLYRCOPCKGEE	543
	::		
480	WAPEGSQTCFPRVTVFLALREHTSVLLAANT	LLLLLLGTAGLFAWHLLDTPVRSAGGR	539
544	WAPEGSQTCFPRVTVFLALREHTSVLLAANT	LLLLLLGTAGLFAWHLLDTPVRSAGGR	603
540	LCFLMLGSLAAGSGSLYGFPGEBTPAPACIL	RQALFALGFTIFLSCLTVRSFQLIIIFKFS	599
604	LCFLMLGSLAAGSGSLYGFPGEBTPAPACIL	RQALFALGFTIFLSCLTVRSFQLIIIFKFS	663
600	TKVPTPYHAWQNHGAGLFWMIS	SSAQQLICLTWLWVWTPLPAREYORPFLWMLSCET	659
664	TKVPTPYHAWQNHGAGLFWMIS	SSAQQLICLTWLWVWTPLPAREYORPFLWMLSCET	723
660	NSLGFILAFLYNGLLSISAFACSYLGKDL	PENYNEAKCVTFSLLFNFSVWIAEFTTASVY	719
724	NSLGFILAFLYNGLLSISAFACSYLGKDL	PENYNEAKCVTFSLLFNFSVWIAEFTTASVY	783
720	DGKYLPAANNMAGLSLSGGFGGYFLPKCYVIL	CRPDNLNTEHFOASIQDYTRRCGST	777
784	DGKYLPAANNMAGLSLSGGFGGYFLPKCYVIL	CRPDNLNTEHFOASIQDYTRRCGST	841

RESULT 2

```

US-09-361-631-1
; Sequence 1, Application US/09361631
; Patent No. 6383778
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Lindemeier, Juergen
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor
; TITLE OF INVENTION: Involved in Sensory Transduction
; FILE REFERENCE: 02307E-088720US
; CURRENT APPLICATION NUMBER: US/09/361,631
; CURRENT FILING DATE: 1999-07-27
; EARLIER APPLICATION NUMBER: US 60/095,464
; EARLIER FILING DATE: 1998-07-28
; EARLIER APPLICATION NUMBER: US 60/112,747
; EARLIER FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 843
; TYPE: PRT
; ORGANISM: Rattus sp.
; FEATURE:
; OTHER INFORMATION: rat G-protein coupled receptor (GPCR) B4 amino
; OTHER INFORMATION: acid sequence
; US-09-361-631-1

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Query Match 31.1%; Score 1288; DB 2; Length 843;
Best Local Similarity 37.7%; Pred. No. 1e-120;
Matches 301; Conservative 142; Mismatches 294; Indels 62; Gaps 22;

Qy	9	GYHLFOAMRLGVBEINNSTALLPNTITLGYQLYDVCDSDANVYATURLVLSLPQGHIEIQG	68
Db	71	GYNLWQAMRFAVEIBINNCSSLLPGVLLGYEMVDVCLSNNH-----PGLYFLAQDD	122
Qy	69	DLL-----HYPSTVLAVIGDSTNRAATTAAALLSPFLV-HISYAASSETLSVQRQPS	120
Db	123	DLLPILKDYSQYMPHVAVIGPDNSESATTVSNILSHFLIPQITYSAISDKLRDKRHPS	182
Qy	121	PLRTIPNDKYQVETNVLVLLOKFGTWTWISLVGSSDDYQGLGVQALENQALVR--GICIAPK	178
Db	183	MLRTVPSATHIEAMVOLMVHFOHNNIIVLVSDDDYGRNSHLL--SORLTKTSDICIAFQ	241

Qy		179	DIMPF--SAQV--GDERMQC--LMRHIAQAAGATVVVVVFSSRQLARVPVPESVLTNLTGVK 233
Db		242	EVLPTPESSQMRSEEQRLDNDLKLRRTSARVVVVFPSPSLYSFFHEVLKRNFTGFV 301
Qy		233	WVASAWALSRIHTGPGIQRIGMVLGAJOKRAVPGLKAFEAAYARADEKA-PRPCHKG 291
Db		302	WTASSEMAIDPVHLNLTRELHRTGTFGLVTTLQRVISIPGPSQFR---VRDKPGVPVENTTN 358
Qy		292	SWCSSNQLCRECOAFAHTMPKLKAFS-----MSS----AYNAVAVTAAVAHLGHOLLGCAS 344
Db		359	LRTTCNQDCDAC-----LNTTKSFNNILLSGERVTVSVZAVATAHAHLRLGCMNR 411
Qy		345	ELCSGRVYVPLLLEQIHVKHYFLHKDTAPANDNRPLSYNNIIANDNGPKWTFVTLGS 404
Db		412	VRECTQKYVYPOLLREIWHVNFTLLGNRLFDDOQGDMPMLLDIIQMWDLSQNPPFOSIAS 471
Qy		405	STWSPVOLNINE-TKIOWHGHNQHVPSKVSSCDLCEGHQRVVTVGFHHCCFECPVCGAGTF 463
Db		472	--YSTSKRELITYINNWSYTPNNTVPVSMCKSQCPQMCKSVGLHPCCFECLDCMGPVY 529
Qy		464	LNKS-ELYRCOPCGTEWABEGSOTCPRPRTVVFUJARLREHTSWV--LLAA-----NTLLLL 516
Db		530	LNRSADFEENCLSCPSSMWXKNDITCQRRPTEFLEWHEVPTIVVAITLAALGFSTLAILF 589
Qy		517	LGITAGLPAWHLDTPVVSAGRLCTLMGLSAAAGSGSLVGGPEGTRPACILLRQALPAL 576
Db		590	-----IFWRHQTPMVRSAGGPCPLMLVPLLLAFMGVPPVVGPTVFCSCRQAPFTV 643
Qy		577	GFTPLSCLTVRSFOLIIIIFKSTKVPTFYHAWQNHGAGLFYMISSAQALLICLTWLVV 636
Db		644	CFSICLSCTIVRSQIVCVPMQARRLSAYSFWMYHGPVVPVAFITAIKVALVUGNMILA 703
Qy		637	WTPLP-AREYORPHLVMLECTETNSIGPIALFYINGLLSISAPACSYLEGKDLPENYNXA 695
Db		704	T TINIGRTHDPDENIMILSCHPNRYRNGLLFNSTMSDLLLSVLGFSAYMGKELPTNYNSA 763
Qy		696	KCVTFSLLPNFVMIAPTTTASVDYGKYLPAANMAG-LSSLGSGGGVPLPKCYVILCR 754
Db		764	KFITLSMTFSTFSSISLCTFMSVHDGVLIYIMDLLVTNLFLAIGL-GYFGPKCYMLIFY 822
Qy		755	PDLNSTEHFOASIODYTRR 773
Db		823	PERNTSAVFNISMIOGYTW 841

RESULT 3

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US-09-897-427A-4
; Sequence 4, Application US/09897427A
; Patent No. 6955887
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; APPLICANT: LI, XIADONG
; APPLICANT: STAZEWSKI, LENA
; APPLICANT: XU, HONG
; APPLICANT: EHEVERRI, FERNANDO
; TITLE OF INVENTION: T1R HETERO-OLIGOMERIC TASTE RECEPTORS
; FILE REFERENCE: 078003-0282558
; CURRENT APPLICATION NUMBER: US/09/897, 427A
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-427A-4

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Query Match 30.6%; Score 1267.5; DB 2; Length 839;
Best Local Similarity 37.4%; Pred. No. 1.2e-118;
Matches 294; Conservative 124; Mismatches 331; Indels 37; Gaps 14;
Cv 9 GYHLFOAMRLGVBEINNSTALLPNITGLGYOLYDVCSDSANVYATLRLVLSFGQHH----IE 65

Db 241 LSRHITGPGIORIGWLVGVAIQKRAVPGKAFEEAYARADKEAPRCHKGSSNQLC 300
Qy 301 RECOAFMAHTMPKLFKAFSSSAYNAYAVAVAHGLHQLLGCASELCSGRVYVWQLLEQ 360
Db 301 RECOAFMAHTMPKLFKAFSSSAYNAYAVAVAHGLHQLLGCASELCSGRVYVWQLLEQ 360
Qy 361 IHKVHFLHLLKDTVAFNDNRDPLSSYNI IAWDNGPKWTFTVLGSSVWSPVQLNINETKI 420
Db 361 IHKVHFLHLLKDTVAFNDNRDPLSSYNI IAWDNGPKWTFTVLGSSVWSPVQLNINETKI 420
Qy 421 WHGKNHQPVSVCSSDCLGEGHQRVVTGFHCCFECVPCGAGTFLNKSLEYRQPCGTEBW 480
Db 421 WHGKNHQPVSVCSSDCLGEGHQRVVTGFHCCFECVPCGAGTFLNKSLEYRQPCGTEBW 480
Qy 481 APEGSTQCPRTVTFALREHTSWVLLAANTLLLLLTAGLFAWHLDTPVVRSAGRL 540
Db 481 APEGSTQCPRTVTFALREHTSWVLLAANTLLLLLTAGLFAWHLDTPVVRSAGRL 540
Qy 541 CFLMLGSLAAGSSLYGFGFEPTRPACLLRQALFALGFTIFLSCLTVRSFQLIIIFKPS 600
Db 541 CFLMLGSLAAGSSLYGFGFEPTRPACLLRQALFALGFTIFLSCLTVRSFQLIIIFKPS 600
Qy 601 KVPFTYHAWQNHGAGLVFMISAAQLLICTLWLVVWVTPLPAREYQRPFLHVMLECTETN 660
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RESULT 2

US-09-927-315-3
; Sequence 3, Application US/09927315
; Publication No. US20030040045A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Ryba, Nicholas J. P.
; APPLICANT: Nelson, Greg
; APPLICANT: Hoon, Mark A.
; APPLICANT: Chandrasekar, Jayaram
; APPLICANT: Zhang, Yifeng
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Mammalian Sweet Taste Receptors
; FILE REFERENCE: 02307E-120110US
; CURRENT APPLICATION NUMBER: US/09/927,315
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/302,898
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 777
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human T1R1 sweet taste receptor
US-09-927-315-3

Query Match 100.0%; Score 4138; DB 3; Length 777;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 RSCSFNEHGYHLFQAMRLGVEEINNSTALLPNTITLGYQLYDVCSDSANVYATLRLVSLPG 60

Qy 61 OHHIELQDGLLHYSPTVLAVIGPDSTNRAATTAALLSPFLVHISYAASSETLSVRQYPS 120
Db 61 OHHIELQDGLLHYSPTVLAVIGPDSTNRAATTAALLSPFLVHISYAASSETLSVRQYPS 120
Qy 121 FLRTIPNDKYQVETVWVLLLOKFGTWTWISLVGSSDDYDGOIGVQALNQALVRGICIAFKDI 180
Db 121 FLRTIPNDKYQVETVWVLLLOKFGTWTWISLVGSSDDYDGOIGVQALNQALVRGICIAFKDI 180
Qy 181 MPFSAQVGDERRMOCLMRHLAQAGATVVVVFSSRQLARVFFESVLTNTLTKGVVASEAWA 240
Db 181 MPFSAQVGDERRMOCLMRHLAQAGATVVVVFSSRQLARVFFESVLTNTLTKGVVASEAWA 240
Qy 241 LSRHITGPGIORIGWLVGVAIQKRAVPGKAFEEAYARADKEAPRCHKGSSNQLC 300
Db 241 LSRHITGPGIORIGWLVGVAIQKRAVPGKAFEEAYARADKEAPRCHKGSSNQLC 300
Qy 301 RECOAFMAHTMPKLFKAFSSSAYNAYAVAVAHGLHQLLGCASELCSGRVYVWQLLEQ 360
Db 301 RECOAFMAHTMPKLFKAFSSSAYNAYAVAVAHGLHQLLGCASELCSGRVYVWQLLEQ 360
Qy 361 IHKVHFLHLLKDTVAFNDNRDPLSSYNI IAWDNGPKWTFTVLGSSVWSPVQLNINETKI 420
Db 361 IHKVHFLHLLKDTVAFNDNRDPLSSYNI IAWDNGPKWTFTVLGSSVWSPVQLNINETKI 420
Qy 421 WHGKNHQPVSVCSSDCLGEGHQRVVTGFHCCFECVPCGAGTFLNKSLEYRQPCGTEBW 480
Db 421 WHGKNHQPVSVCSSDCLGEGHQRVVTGFHCCFECVPCGAGTFLNKSLEYRQPCGTEBW 480
Qy 481 APEGSTQCPRTVTFALREHTSWVLLAANTLLLLLTAGLFAWHLDTPVVRSAGRL 540
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Db 541 CFLMLGSLAAGSSLYGFGFEPTRPACLLRQALFALGFTIFLSCLTVRSFQLIIIFKPS 600
Qy 601 KVPFTYHAWQNHGAGLVFMISAAQLLICTLWLVVWVTPLPAREYQRPFLHVMLECTETN 660
Db 601 KVPFTYHAWQNHGAGLVFMISAAQLLICTLWLVVWVTPLPAREYQRPFLHVMLECTETN 660
Qy 661 SLGFIAPLYNGLLSISAFACSVLKGDLPENYNEAKCVTFSLFNFVSWIAFTTASVVD 720
Db 661 SLGFIAPLYNGLLSISAFACSVLKGDLPENYNEAKCVTFSLFNFVSWIAFTTASVVD 720
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Db 721 GKYLPAANMAGLSLSGSGGFGYFLPKCVYILCRDLNSTEHFQASIQDYTRCGST 777

RESULT 3

US-10-190-417-3
; Sequence 3, Application US/10190417
; Publication No. US20030166137A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Ryba, Nicholas J. P.
; APPLICANT: Chandrasekar, Jayaram
; APPLICANT: Hoon, Mark A.
; APPLICANT: Nelson, Greg
; APPLICANT: Zhang, Yifeng
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Mammalian Sweet and Amino Acid Heterodimeric Taste
; FILE REFERENCE: 02307E-120130US
; CURRENT APPLICATION NUMBER: US/10/190,417
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: US 60/302,898
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 09/927,315

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 14:54:39 ; Search time 14.8512 Seconds
(without alignments)
2421.578 Million cell updates/sec

Title: US-09-361-652-3
Perfect score: 4138
Sequence: 1 RSCSPFNEGHVHLFQAMRLGV.....NSTEHFQASIQDYTRRCGST 777

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /SIDSS/ptodata/2/pubpaa/US06 NEW PUB.pep1:
2: /SIDSS/ptodata/2/pubpaa/US06 NEW PUB.pep2:
3: /SIDSS/ptodata/2/pubpaa/US07 NEW PUB.pep:
4: /SIDSS/ptodata/2/pubpaa/US08 NEW PUB.pep:
5: /SIDSS/ptodata/2/pubpaa/US09 NEW PUB.pep:
6: /SIDSS/ptodata/2/pubpaa/US09 NEW PUB.pep:
7: /SIDSS/ptodata/2/pubpaa/US10 NEW PUB.pep1:
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12: /SIDSS/ptodata/2/pubpaa/US60 NEW PUB.pep2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	4138	100.0	777	9	US-10-645-441-3
2	4064.5	98.2	841	9	US-10-725-475-5
3	4064.5	98.2	841	11	US-11-050-804-2
4	3154.5	76.2	840	9	US-10-645-441-1
5	3154.5	76.2	840	9	US-10-725-475-16
6	3104.5	75.0	842	9	US-10-645-441-2
7	1288	31.1	843	9	US-10-725-475-17
8	1288	31.1	843	9	US-10-645-441-9
9	1270	30.7	838	9	US-10-725-475-6
10	1267.5	30.6	839	11	US-11-050-804-4
11	1267.5	30.6	843	9	US-10-645-441-8
12	1258.5	30.4	838	9	US-10-645-441-25
13	1075.5	26.0	858	9	US-10-725-475-4
14	1075.5	26.0	858	9	US-10-645-441-23
15	1060.5	25.6	858	9	US-10-645-441-18
16	1059.5	25.6	858	9	US-10-725-475-7
17	1056	25.5	852	9	US-10-645-441-15
18	1053	25.4	852	9	US-11-050-804-6
19	1053	25.4	852	11	US-11-050-804-6
20	1047.5	25.3	858	9	US-10-645-441-20
21	1029.5	24.9	867	9	US-10-725-475-19

22	1000.5	24.2	928	9	US-10-841-129-4	Sequence 4, Appl1
23	981.5	23.7	928	9	US-10-841-129-6	Sequence 6, Appl1
24	932.5	22.5	926	9	US-10-841-129-2	Sequence 2, Appl1
25	676.5	16.3	1199	9	US-10-922-166-15	Sequence 15, Appl1
26	672.5	16.3	845	9	US-10-725-475-18	Sequence 18, Appl1
27	656.5	15.9	879	9	US-10-877-346-52	Sequence 52, Appl1
28	655.5	15.8	879	9	US-10-877-346-53	Sequence 53, Appl1
29	655.5	15.8	879	9	US-10-877-346-54	Sequence 54, Appl1
30	654.5	15.8	879	9	US-10-877-346-17	Sequence 17, Appl1
31	643.5	15.6	865	11	US-11-094-519A-41	Sequence 41, Appl1
32	479.5	11.6	242	9	US-10-725-475-13	Sequence 13, Appl1
33	440.5	10.6	497	9	US-10-918-857-8	Sequence 8, Appl1
34	440.5	10.6	576	9	US-10-922-166-2	Sequence 2, Appl1
35	440.5	10.6	790	9	US-10-918-857-6	Sequence 6, Appl1
36	440.5	10.6	790	9	US-10-922-166-20	Sequence 20, Appl1
37	403	9.7	425	9	US-10-918-857-4	Sequence 4, Appl1
38	403	9.7	718	9	US-10-918-857-2	Sequence 2, Appl1
39	383.5	9.3	256	9	US-10-877-346-85	Sequence 85, Appl1
40	354	8.6	236	9	US-10-725-475-15	Sequence 15, Appl1
41	337	8.1	165	9	US-10-725-475-14	Sequence 14, Appl1
42	307.5	7.4	137	9	US-10-725-475-12	Sequence 12, Appl1
43	259	6.3	402	9	US-10-877-346-84	Sequence 84, Appl1
44	181	4.4	844	11	US-11-127-877-40	Sequence 40, Appl1
45	138	3.3	885	9	US-10-912-971-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1

US-10-645-441-3
; Sequence 3, Application US/10645441
; Publication No. US20050260599A1
; GENERAL INFORMATION:
; APPLICANT: Zuber, Charles S.
; APPLICANT: Ryba, Nicholas J.P.
; APPLICANT: Nelson, Greg
; APPLICANT: Hoon, Mark A.
; APPLICANT: Chandrasekar, Jayaram
; APPLICANT: Zhang, Yifeng
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Mammalian Sweet Taste Receptors
; FILE REFERENCE: 023078-120110US
; CURRENT APPLICATION NUMBER: US/10/645,441
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: US/09/927,315
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/302,898
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 3
; LENGTH: 777
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human T1R1 sweet taste receptor
US-10-645-441-3

Query Match 100.0%; Score 4138; DB 9; Length 777;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	RSCSPFNEGHVHLFQAMRLGVVEEINNSTALLPNTITLGVLYDVCSDSNVYATLRVLSLPG	60
Db	1	RSCSPFNEGHVHLFQAMRLGVVEEINNSTALLPNTITLGVLYDVCSDSNVYATLRVLSLPG	60
Qy	61	QHIEHQLQDILLHYSPVTLAVIGPDSNTNRAATTAALLSPFLVHISYAASSTLTSVKQYPS	120
Db	61	QHIEHQLQDILLHYSPVTLAVIGPDSNTNRAATTAALLSPFLVHISYAASSTLTSVKQYPS	120

121 FLRTIPNDKYOVETWVLLLOKQGTWISLVGSSDDYQGLGVQALENOALVRGICIAFKDI 180
121 FURTPNDKYOVETWVLLLOKQGTWISLVGSSDDYQGLGVQALENOALVRGICIAFKDI 180
181 MPFSAQVGDQMRQCLMRHLAQAGATVVVFSRQLARVFFESVLTNLTKGVWVASEAWA 240
181 MPFSAQVGDQMRQCLMRHLAQAGATVVVFSRQLARVFFESVLTNLTKGVWVASEAWA 240
241 LSRHITGVPGIQRIGMVLGVAIQRAVPGIKAFEEYARADKEAPRCHKGSCSNQJLC 300
241 LSRHITGVPGIQRIGMVLGVAIQRAVPGIKAFEEYARADKEAPRCHKGSCSNQJLC 300
301 RECQAFMAHTMPKIKAFSSSSAYNAYAVAVAHGLHQLGACSELCSGRVYVPMQLLEQ 360
301 RECQAFMAHTMPKIKAFSSSSAYNAYAVAVAHGLHQLGACSELCSGRVYVPMQLLEQ 360
361 IHKVHFLHLDKDTVAFNDNRDPLSSYNI IAWDMNGPKWTFTVLGSSSTWSPVQLNINETKIQ 420
361 IHKVHFLHLDKDTVAFNDNRDPLSSYNI IAWDMNGPKWTFTVLGSSSTWSPVQLNINETKIQ 420
421 WHGKNHQPVSVCSSDCLSGHQVVTGPHHCCPECVPCGAGTFLNKSLEYRCQPCGTEBW 480
421 WHGKNHQPVSVCSSDCLSGHQVVTGPHHCCPECVPCGAGTFLNKSLEYRCQPCGTEBW 480
481 APEGSTQCFPRTPVFLALREHTSWVLLAANTLLILLGLCTAGLFAWHLDTVPVRSAGRL 540
481 APEGSTQCFPRTPVFLALREHTSWVLLAANTLLILLGLCTAGLFAWHLDTVPVRSAGRL 540
541 CFLMLGSLAAGSGSLYGFGEPTRPACLLRQALFALGFTIFLSCLTVRSFQLIIPKFT 600
541 CFLMLGSLAAGSGSLYGFGEPTRPACLLRQALFALGFTIFLSCLTVRSFQLIIPKFT 600
601 KVPTFTYHAWVQNHGAGLFVMISSAAQLLICLTWLVVWVTPLPAREYORPFLHVMLECTETN 660
601 KVPTFTYHAWVQNHGAGLFVMISSAAQLLICLTWLVVWVTPLPAREYORPFLHVMLECTETN 660
661 SLGFTILAFYNGLLSISAFACSYLGHKOLPENYNEAKCVTFSLFNFVSWIAFFTASVYD 720
661 SLGFTILAFYNGLLSISAFACSYLGHKOLPENYNEAKCVTFSLFNFVSWIAFFTASVYD 720
721 GKYLPAANMAGLSLSSGGFGYFLPKCYVILCRPDLNSTEHFQASIQDYTRRCGST 777
721 GKYLPAANMAGLSLSSGGFGYFLPKCYVILCRPDLNSTEHFQASIQDYTRRCGST 777

RESULT 2

US-10-725-475-5
; Sequence 5, Application US/10725475
; Publication No. US20060014208A1
; GENERAL INFORMATION:
; APPLICANT: ZOLLER, MARK
; APPLICANT: LI, XIAODONG
; APPLICANT: STASZEWSKI, LENA
; APPLICANT: O'CONNELL, SHAWN
; APPLICANT: ZOZULYA, SERGEY
; APPLICANT: ADLER, JON
; APPLICANT: XU, HONG
; APPLICANT: ECHEVERRI, FERNANDO
; TITLE OF INVENTION: TIR HETERO-OLIGOMERIC TASTE RECEPTORS AND CELL LINES
; TITLE OF INVENTION: TIR HETERO-OLIGOMERIC TASTE RECEPTORS AND USE THEREOF FOR
; TITLE OF INVENTION: IDENTIFICATION OF TASTE COMPOUNDS
; FILE REFERENCE: 078003-0291566
; CURRENT APPLICATION NUMBER: US/10/725,475
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/300,434
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/304,749
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/310,493
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/331,771
; PRIOR FILING DATE: 2001-11-21

; PRIOR APPLICATION NUMBER: 60/339,472
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/372,090
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: 60/374,143
; PRIOR FILING DATE: 2002-04-22
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 841
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-725-475-5

Query Match 98.2%; Score 4064.5; DB 9; Length 841;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 766; Conservative 5; Mismatches 1; Gaps 1;
QY 1 RSCSFNEHGYHLFOAMRLGVEBEINNSTALLPNTILGYQLYDVCSDSANVYATLRLVSLPG 60
DB 64 RSCSFNEHGYHLFOAMRLGVEBEINNSTALLPNTILGYQLYDVCSDSANVYATLRLVSLPG 123
QY 61 QHHIELQGDLLHYSTVLAVIGPDSNRAATTAALLSPFLV-HIISYAAASSETLSVKRQYP 119
DB 124 QHHIELQGDLLHYSTVLAVIGPDSNRAATTAALLSPFLVPMISYAAASSETLSVKRQYP 183
QY 120 SFLRTIPNDKYOVETWVLLLOKQGTWISLVGSSDDYQGLGVQALENOALVRGICIAFKD 179
DB 184 SFLRTIPNDKYOVETWVLLLOKQGTWISLVGSSDDYQGLGVQALENOALVRGICIAFKD 243
QY 180 IMPFSAQVGDQMRQCLMRHLAQAGATVVVFSRQLARVFFESVLTNLTKGVWVASEAW 239
DB 244 IMPFSAQVGDQMRQCLMRHLAQAGATVVVFSRQLARVFFESVLTNLTKGVWVASEAW 303
QY 240 ALSRHTGVPGIQRIGMVLGVAIQRAVPGIKAFEEYARADKEAPRCHKGSCSNQJLC 299
DB 304 ALSRHTGVPGIQRIGMVLGVAIQRAVPGIKAFEEYARADKEAPRCHKGSCSNQJLC 363
QY 300 CRECOAFMAHTMPKIKAFSSSSAYNAYAVAVAHGLHQLGACSELCSGRVYVPMQLLE 359
DB 364 CRECOAFMAHTMPKIKAFSSSSAYNAYAVAVAHGLHQLGACSELCSGRVYVPMQLLE 423
QY 360 QHKKVHFLHLDKDTVAFNDNRDPLSSYNI IAWDMNGPKWTFTVLGSSSTWSPVQLNINETKI 419
DB 424 QHKKVHFLHLDKDTVAFNDNRDPLSSYNI IAWDMNGPKWTFTVLGSSSTWSPVQLNINETKI 483
QY 420 QHKKVHFLHLDKDTVAFNDNRDPLSSYNI IAWDMNGPKWTFTVLGSSSTWSPVQLNINETKI 479
DB 484 QHKKVHFLHLDKDTVAFNDNRDPLSSYNI IAWDMNGPKWTFTVLGSSSTWSPVQLNINETKI 543
QY 480 WAPEGSTQCFPRTPVFLALREHTSWVLLAANTLLILLGLCTAGLFAWHLDTVPVRSAGRL 539
DB 544 WAPEGSTQCFPRTPVFLALREHTSWVLLAANTLLILLGLCTAGLFAWHLDTVPVRSAGRL 603
QY 540 LCFLMLGSLAAGSGSLYGFGEPTRPACLLRQALFALGFTIFLSCLTVRSFQLIIPKFT 599
DB 604 LCFLMLGSLAAGSGSLYGFGEPTRPACLLRQALFALGFTIFLSCLTVRSFQLIIPKFT 663
QY 600 TKVPTFTYHAWVQNHGAGLFVMISSAAQLLICLTWLVVWVTPLPAREYORPFLHVMLECTET 659
DB 664 TKVPTFTYHAWVQNHGAGLFVMISSAAQLLICLTWLVVWVTPLPAREYORPFLHVMLECTET 723
QY 660 NSLGFILAFYNGLLSISAFACSYLGHKOLPENYNEAKCVTFSLFNFVSWIAFFTASVY 719
DB 724 NSLGFILAFYNGLLSISAFACSYLGHKOLPENYNEAKCVTFSLFNFVSWIAFFTASVY 783
QY 720 DGKYLPAANMAGLSLSSGGFGYFLPKCYVILCRPDLNSTEHFQASIQDYTRRCGST 777
DB 784 DGKYLPAANMAGLSLSSGGFGYFLPKCYVILCRPDLNSTEHFQASIQDYTRRCGST 841

RESULT 3

US-11-050-804-2